seq_documentation_block:
; Sequence 15, Application US/09376770
; GENERAL INFORMATION:
; APPLICANT: Murdin, Andrew
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 19721-006
; CURRENT APPLICATION NUMBER: US/09/376,770
; CURRENT FILING DATE: 1999-08-17
; EARLIER APPLICATION NUMBER: 60/097,187
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/097,188
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/097,189
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/097,190
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/097,187
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/097,195
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/097,196
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/097,197
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/097,191
; EARLIER FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 2957
; TYPE: DNA
; ORGANISM: Chlamydia sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(2854)
US-09-376-770-15

Align seq 1/1 to: US-09-376-770-15 from: 1 to: 2957

alignment_block:
US-09-428-122-2 x US-09-376-770-15

alignment_scores:
          Quality: 2006.00   Length: 948
          Ratio: 2.810   Gaps: 20
Percent Similarity: 75.316   Percent Identity: 45.570

  1 MetLysSerSerPheProLysPheValPheSerThrPheAlaIlePhePr 17
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101 ATGAGAACTCGTCTTTTTCCTTGTTATTAATATCTTCATCTCTAGCCTTTCC 150

 17 oLeuSerMetIle..........AlaThrGlyThrValIleuAspSerS 30
    |||| ||| |||:::||| ::|||| :::||| |||
150 ....

151 TCTCTTAATGAGTGTTTCTCCGAGATGCTGCGGATCTCACATTAGGGAGTC 200
 30 erAlaSerPheAspGlyAsn....LysAsnGlyAsnPheSerValArgGlu 45
    |||:||::| |||:::   ::|||:|::   ::::||| :::|||
201 GTGACAGTTATAAATGGTGATAACAGCAACCACAGAATTACtCCTAAAGCG 250

 46 SerGlnGluAspAla....GlyThrThrTyrLeuPheLysC::AsnValTh 61
    ::: |||||||||:::||| ::||:|||: |:|
251 GCAACTTCTGATGCTAGTGCGCACGACCTATATtCCtGATGGGATGTCTC 300

 61 rLeuGluAsnIleProGlyThrGlyThrThrAlaIleThrLysSerCysPh 79
    :::||||||||||||| |||:||||||:::   :::||| ||:|||
301 GATAACCCAA...GCAGGGAAACAAACGAGCTTAACCACAACGTTGTTTTT 347

 78 snAsnThrLysGlyAspLeuThrPheThrGlyAsnGlyAsnSerLeuLeu 94
    ::::||||||| :::||||||| :::|||||||:||| |||||||
348 CTAACACTGCAGGAAAATCTTACCTTCTTAGGGAACAGGATTTTCTTCAt 397

 95 PheGlnThrValAspAlaGlyThrValAlaGlyIleAlaAlaValAsnSerSe 111
    ::||||||||| :::|||||||::: :::|||||||:||
398 TTTGACAATAATATTCGTCTACGTTGCAGGTGTTGTTGTTAGCAATAC 447

111 rValValAspLysSerThrThrPheIleGlyPheSerSerLeuSerPheI 128
    |||:|::::|| ||| :::||| :::||||||| ||:|||
448 AGCAGCTTCTGGCGATACGAAATTCTCAGGATTTCAACTCTCGGATGC 497

128 leAlaSerProGlySerSerIleThrThrGlyLysGlyAlaValSerCys 144
    :::|||:||| :::::: ||| :::|||||||
498 TTGCAGCTCCTAGG......ACCACAGGTAAAGGAGGCCAtTAAAATt 538

145 SerThrGlySerLeuSerLeuThrLysAsnValSerLeuLeuPheSerLy 161
    ||||||| :::|||:||| |||:|::||| :::|||||||
539 ACCGGATGGT...CTGGTGTTGGAGTATAGGGAATTCGATCTTAAtGA 585

161 sAsnPheSerThrAspAsnGlyValAsnAlaIleThrAlaLysThrLeuThr 178
    :::|||||||||||| :::|||||||:|||||||||||:::|||
585 AAATGCCTCTACTGAAAATGGGGAGCCATCAAATACGAAGACTTTGTCTT 635

178 euThrGlyThrThrMetSerAlaLeuPheSerGluAsnThrSerSerLys 194
    ||||||||||| ||| :::|||:::|||||||:|::|||
636 TGACTGGGAGTACGGCGGTTGTTAGCCTTCCTTGGCAAATAGCCTCGCCAA 685

195 LysSerGlyGlyAlaIleGlyIleThrSerAspAlaLeuThrIleThrGlyAsnGl 211
    |||:|::||| |||:::||| ||||||| :::|||||||
686 CAAGGGGGAGCCGAATCTATGCTTCGGTGACTCTGGATTCTGAGAATGC 735

211 nGlyGluValSerPheSerAspAsnThrSerSerAspSerGlyAlaAlaIle 228
    :::||||||| ||| :::|||:|||||| |||:|| |||:|::
736 AGGAAATCTTGAGCTTCGGAACAACACTGCGACAACATCAGGAGGCCGA 785

228 lePheThrGluAlaSerValThrIleSerAsnAsnAlaLysValSerPhe 244
    ||| ::|||||| :::||| |||||||:|::
786 TCTCTGCTTGAAGGGAACCTTGTGATCTCCAATAACCAAAAATATCTTTTC 835

245 IleAspPhelysValThrGlyAlaSerSerSerThrThrGlyAspMetSe 261
    :::||| ::::|||||| ::::::|||||||||||
836 GATGGCTGCAAAGCAACT..........................ACAAA 858

261 rGlyGlyAlaIleGlyCysAlaTyrLys.......ThrSerThrAspThrLysSv 276
    :::|||:::|||::::::: :::||| :::|||||||:|:
859 TGGCGGAGCTATTGAtTGTAACAAAGCAGGGGGAACCAGACCCTATCt 908

276 alThrLeuThrGlyAsnGlnMetLeuLeuPheSerAsnAsnThrSerThr 292
    :::||||||| :::||| ||| ||| ::::::|||
909 TGACTCTTTCAGGAAATGAGCAGCCTGCATTTCTGAATAACACAGCAGGA 958

293 ThrAlaGlyGlyAlaIleTyrValLysLysLeuGluLeuAlaSerGly... 308
    :::|||:|||:|| :::||| :::||| :::|||
959 AATAGTGGAGGTCGATTTATACCAAAAAAATTGGTGTTAGCCTCAGGACG 1008

309 .GlyLeuThrLeuPheSerArgAsnSerValAsnGlyGlyThrAlaPro L 325
    ||| :::||||||| ::::||||||:|||||||||||::: |||
1009 AGGAGGAGTGTTATTTTCTAACAACAAAAGCTCGGAATGCTACT...CCIA 1055

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AC       P71133;
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DT       01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT       01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE       POMP91B PRECURSOR.
OS       Chlamydophila psittaci.
OC       Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
RN       [1]
RP       SEQUENCE FROM N.A.
RC       STRAIN=OVINE ENZOOTIC ABORTION ISOLATE S26/3;
RX       MEDLINE; 96406378.
RA       Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.;
RT       "Identification of a multigene family coding for the 90 kDa proteins
RT       of the ovine abortion subtype of Chlamydia psittaci.";
RL       FEMS Microbiol. Lett. 142:277-281(1996).
RN       [2]
RP       SEQUENCE FROM N.A.
RC       STRAIN=OVINE ENZOOTIC ABORTION ISOLATE S26/3;
RX       MEDLINE; 98187897.
RA       Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
RT       "Molecular cloning and characterization of the genes coding for the
RT       highly immunogenic cluster of 90-kilodalton envelope proteins from the
RT       Chlamydia psittaci subtype that causes abortion in sheep.";
RL       Infect. Immun. 66:1317-1324(1998).
DR       EMBL; U65943; AAC15923.1; -.
KW       Signal.
FT       SIGNAL        1     16       POTENTIAL.
FT       CHAIN        17    846       POMP91B.
SQ       SEQUENCE   846 AA;  90834 MW;  4CDC31DC03C2964E CRC64;
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Query Match
Best Local Similarity   33.6%;
                        38.7%;   Score 1604.5; DB 2; Length 846;
Matches 368; Conservative 140; Pred. No. 1.8e-82;
                                   Pred. No. 1.8e-82; Mismatches 269; Indels 173; Gaps 26;

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Qy     23 TETVLDSSASFDGN-KNGNFSVRESQEDAGTTYLFKGNVTLENIPGTGTAITKSCPNNTK     81
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Db     26 TNETLTSSDSYNGNVTSDEFEVKET--TSGAIYTCEGNVCI-SYAGKDSPLNKSCFSETT   82

Qy     82 GDLTFTGNGNSLLFQTVDAGTVAGAAVNSSVVDKSTTFIGFS--SLSFIASPGSSTTTGK    139
             :|:|| ||||| :| | || | || |   ||| |||:|||    ||| |||| |||: |
Db     83 ENLSFIGNGYICFDNITTQSSHPGAISVSGTNKTLDISGFSLFSCAYCCPPG--TTGY    139

Qy    140 GAVSCSTGSLSLTKNVSLLFSKNFSIDNGAITAKILSLIGTTMSALFSENTSSKKGGAI    199
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Db    140 GAIQ-TKGTTLKDNSSLVFHKNCSTAEGGAIQCK--------------------------    173

Db    200 QTSDALITIGNQGEVSFSDNTSSDSGAAIFEASVTISNNAKVSFIDNKVTGASSSTTGD    259
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                                                      ----SSSSTAE    180

Db    260 MSGGAICAYKTSTDTKVTLTGNQMLLFSNNTSTTAGGAIVKKLELASGGLTLFSRNSVN    319
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Qy    181 LK---------LENNKNLVFSENSSKERGGAIYADKLTIVSGGPTLFSNNSVS    224

Db    320 GGTAPKGGAIAIEDS--GELSLSADSGDIVFLGNTVTST----TPGTNRSSIDLGTSAKMTA    375
             |||| ||||| ||    | | ||||| ||| || | |      ||||| |||||  |||
Qy    225 HNSSPKGGAICIKDSDGECSLTANLGDIIFDGNKIIITNGGSPTVTRNSIDLGSGGKFTK    284

Db    376 LRSAAGRAIYFYDPI-TTGSSTTVDDVLKYNETPADSALQYTGNIIFIGEKLSETEAADS    434
             |::| | ||  ||   |||:|| |  ||  | ||:  |  |:|    ||| || |
Qy    285 LNAKEGFGIFFYDPIANTGGSTEI---ELNKTESDTT--YTGKIVFSGEKLSDEEKTVP    338

Db    435 KNLTSKLLQPVTLSGGTLSLSKHGYTLQTQAFTQQADSRLEMDVGTTLE----PADTSTIN    490
             |||:|||||| ||| | | ||| | || | | ||||:| || |  | |     | ||
Qy    339 ANLKSYFKQPLKIGAGSLVLKDGVTLEARKIITQTKGSTVVMDLGTTLQTPSSSGETITLT    398

Db    491 NLVINISSI---DGAKKAKIETKRATSKNLTLSGTTILLDPTGTGTFYENNSLRNPQSYDILE    547
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Qy    399 NLDINIASLGGGGGTAPAKLATNTPASOAISIA-AVNLVNTDSNTYEDPILSRASKSFSAI-    456

Db    548 LKASGTVTSTAVTPDPIMGEKF----HYGVQGTWGPIVWGTGAST---TAFFNWTKIGYI    600
             || ||||:| |  | ||  ||        |  | | || ||| ||      | |||:|
Qy    457 ---TATTSSSTVIPPETNLKNYIPPTHYGYQGNW-TVTWKQGSSAQEKTATLTWEQYGYS    512

Db    601 PNPERIGSLVPNSLWNAFIDISSLHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKTRRG    660
             ||| | ||||| |: |  | |:||||||| ||||||||| | |||||||||:|:|||:|
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Db    661 FRHLSGGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFVAKNQGTVVGGTLYYQHNETYIS    720
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Qy    573 FRHHSAGYALGVTAQOTPSDDVCSAAFCQLFGKDKDYFVSKNSSTIYAGSIYYQH------    626

Db    721 LPCKLRPCSLSVPT---------EIPVLFSGNLSYTHIDNDLKTKYT---------TY    761
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Qy    627 ----------ISVWNTWNTLLQNTLGAEAPLVLNAQLTYCHASNNMKTNMTNTYTPKNVTP    677

Db    762 PTVKGSWGNDSFALEFGGRAPICLDESALFEQYMPFNKLQTVVAHQEGFKEQGT-EAREF    820
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Qy    678 SEIKGDWGNDCFGVEFGAKAPI-ETASLLFDMYSPFVKLQLVHAHQDDFKENNSDQGRYF    736

Db    821 GSSRLVNLALPTGIRFDKESDCQDATYNLTLGYTVDLVRSNPDCTTTLRISGDS--WKTF    878
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Qy    737 ESNNLTNLSMPIGVKLEKFSHKDTASYNLTLAYAPDIVRSNPDCTASLLVSPTSAVWVIK    796

Db    879 GTNLARQALVLRAGNHFCFNSNFEAFSQFSFELRGSSRNNNVDLGAKYQF    928
             |||| |   :|| ||  |  ||| |  |  ||||||:|:|||| |  ||
Qy    797 ANNLARHAFILQAGNYLALTRNTELFSQFGFELRGSCRTYNIDLGSKIQF    846
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RESULT 13